SEQUENCE LISTING

<110> SmithKline Beecham Biologicals S.A.

<120> Novel Compounds

<130> BM45412

<160> 10

<170> FastSEQ for Windows Version 3.0

<210> 1
<211> 1509
<212> DNA
<213> *Moraxella catarrhalis*

<400> 1

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agtggttgta gcaatcaagc ggacaaagcc gcccagccaa aaagcagcac ggtagacgct     120
gccgccaaga cagcaaatgc agataatgct gcctcacaag aacatcaagg cgagctgcct     180
gtcattgatg ccattgttac gcatgcacca gaagttccac cacctgttga ccgtgaccac     240
cccgccaaag tggtggtaaa aatggaaacc gttgaaaaag tcatgcgtct ggcagatggc     300
gtggaatatc agttttggac atttggcggt caagttccag ggcagatgat tcgtgtgcgt     360
gaaggcgaca ccatcgaagt gcagttctca aaccacccag attcaaaaat gccccataat     420
gttgactttc acgctgccac agggcctggc ggcggggcag aagcgtcatt taccgcaccg     480
ggtcatacat caacctttag ttttaaagcc ttacagcctg gtttgtatgt ctatcactgt     540
gcggttgccc ctgttggcat gcacattgct aatggcatgt atggtttgat tttggttgaa     600
ccaaaagagg gcttgccaaa agtagataaa gaatactatg tcatgcaagg cgacttttat     660
accaaaggca aatatggcga acaaggtcta cagccctttg atatggaaaa agccattcga     720
gaagatgctg aatatgttgt ctttaatggt tcggtggggg cgttgactgg tgaaaatgct     780
ctaaaagcca aggttggcga aactgttcgc ttatttgtgg gtaacggcgg cccgaatttg     840
acatcatcat tccatgtcat tggtgagatt tttgataagg ttcactttga gggtggtaag     900
ggtgaaaacc acaatatcca aaccacgcta atcccagcag gtggcgctgc catcactgaa     960
tttaaggtgg atgtgccggg tgattatgtc ttggttgacc atgccatctt ccgtgccttt    1020
aacaaagggg cattgggcat acttaaggtg gaaggtgaag aaaatcatga gatttattca    1080
cacaaacaaa cagacgctgt ctatctgcca gagggtgccc cacaagcaat tgatacccaa    1140
gaagcaccca aaacacctgc acctgccaac ttacaagagc agattaaagc aggtaaggca    1200
acctatgact ctaactgtgc tgcttgtcac caacctgatg gtaaaggcgt gccaaacgct    1260
ttcccaccgc ttgccaactc tgactatctg aacgccgacc acgctcgtgc cgccagcatc    1320
gtggcaaatg gattgtctgg taagattacc gtcaatggca accaatatga aagcgtcatg    1380
cctgcgattg ctctgagcga ccaacagatt gccaatgtca tcacctacac gcttaacagc    1440
tttggtaaca aaggcggtca actcagtgca gacgatgtgg caaaagccaa aaaaaccaag    1500
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<210> 2
<211> 502
<212> PRT
<213> *Moraxella catarrhalis*

<400> 2

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 1               5                  10                  15
Ala Leu Met Leu Ser Gly Cys Ser Asn Gln Ala Asp Lys Ala Ala Gln
            20                  25                  30
Pro Lys Ser Ser Thr Val Asp Ala Ala Ala Lys Thr Ala Asn Ala Asp
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        35                  40                  45
Asn Ala Ala Ser Gln Glu His Gln Gly Glu Leu Pro Val Ile Asp Ala
    50                  55                  60
Ile Val Thr His Ala Pro Glu Val Pro Pro Pro Val Asp Arg Asp His
65                  70                  75                  80
Pro Ala Lys Val Val Val Lys Met Glu Thr Val Glu Lys Val Met Arg
                85                  90                  95
Leu Ala Asp Gly Val Glu Tyr Gln Phe Trp Thr Phe Gly Gly Gln Val
            100                 105                 110
Pro Gly Gln Met Ile Arg Val Arg Glu Gly Asp Thr Ile Glu Val Gln
        115                 120                 125
Phe Ser Asn His Pro Asp Ser Lys Met Pro His Asn Val Asp Phe His
    130                 135                 140
Ala Ala Thr Gly Pro Gly Gly Gly Ala Glu Ala Ser Phe Thr Ala Pro
145                 150                 155                 160
Gly His Thr Ser Thr Phe Ser Phe Lys Ala Leu Gln Pro Gly Leu Tyr
                165                 170                 175
Val Tyr His Cys Ala Val Ala Pro Val Gly Met His Ile Ala Asn Gly
            180                 185                 190
Met Tyr Gly Leu Ile Leu Val Glu Pro Lys Glu Gly Leu Pro Lys Val
        195                 200                 205
Asp Lys Glu Tyr Tyr Val Met Gln Gly Asp Phe Tyr Thr Lys Gly Lys
    210                 215                 220
Tyr Gly Glu Gln Gly Leu Gln Pro Phe Asp Met Glu Lys Ala Ile Arg
225                 230                 235                 240
Glu Asp Ala Glu Tyr Val Val Phe Asn Gly Ser Val Gly Ala Leu Thr
                245                 250                 255
Gly Glu Asn Ala Leu Lys Ala Lys Val Gly Glu Thr Val Arg Leu Phe
            260                 265                 270
Val Gly Asn Gly Gly Pro Asn Leu Thr Ser Ser Phe His Val Ile Gly
        275                 280                 285
Glu Ile Phe Asp Lys Val His Phe Glu Gly Gly Lys Gly Glu Asn His
    290                 295                 300
Asn Ile Gln Thr Thr Leu Ile Pro Ala Gly Gly Ala Ala Ile Thr Glu
305                 310                 315                 320
Phe Lys Val Asp Val Pro Gly Asp Tyr Val Leu Val Asp His Ala Ile
                325                 330                 335
Phe Arg Ala Phe Asn Lys Gly Ala Leu Gly Ile Leu Lys Val Glu Gly
            340                 345                 350
Glu Glu Asn His Glu Ile Tyr Ser His Lys Gln Thr Asp Ala Val Tyr
        355                 360                 365
Leu Pro Glu Gly Ala Pro Gln Ala Ile Asp Thr Gln Glu Ala Pro Lys
    370                 375                 380
Thr Pro Ala Pro Ala Asn Leu Gln Glu Gln Ile Lys Ala Gly Lys Ala
385                 390                 395                 400
Thr Tyr Asp Ser Asn Cys Ala Ala Cys His Gln Pro Asp Gly Lys Gly
                405                 410                 415
Val Pro Asn Ala Phe Pro Pro Leu Ala Asn Ser Asp Tyr Leu Asn Ala
            420                 425                 430
Asp His Ala Arg Ala Ala Ser Ile Val Ala Asn Gly Leu Ser Gly Lys
        435                 440                 445
Ile Thr Val Asn Gly Asn Gln Tyr Glu Ser Val Met Pro Ala Ile Ala
    450                 455                 460
Leu Ser Asp Gln Gln Ile Ala Asn Val Ile Thr Tyr Thr Leu Asn Ser
465                 470                 475                 480
Phe Gly Asn Lys Gly Gly Gln Leu Ser Ala Asp Asp Val Ala Lys Ala
                485                 490                 495
Lys Lys Thr Lys Pro Asn
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500

<210> 3
<211> 1506
<212> DNA
<213> *Moraxella catarrhalis*

<400> 3

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agtggttgta gcaatcaagc ggacaaagcc gcccagccaa aaagcagcac ggtagacgct     120
gccgccaaga cagcaaatgc agataatgct gcctcacaag aacatcaagg cgagctgcct     180
gtcattgatg ccattgttac gcatgcacca gaagttccac cacctgttga ccgtgaccac     240
cccgccaaag tggtggtaaa aatggaaacc gttgaaaaag tcatgcgtct ggcagatggc     300
gtggaatatc agttttggac atttggcggt caagttccag ggcagatgat tcgtgtgcgt     360
gaaggcgaca ccatcgaagt gcagttctca aaccacccag attcaaaaat gccccataat     420
gttgactttc acgctgccac agggcctggc ggcggggcag aagcgtcatt taccgcaccg     480
ggtcatacat caacctttag ttttaaagcc ttacagcctg gtttgtatgt ctatcactgt     540
gcggttgccc ctgttggcat gcacattgct aatggcatgt atggtttgat tttggttgaa     600
ccaaaagagg gcttgccaaa agtagataaa gaatactatg tcatgcaagg cgacttttat     660
accaaaggca aatatggcga acaaggtcta cagccctttg atatggaaaa agccattcga     720
gaagatgctg aatatgttgt ctttaatggt tcggtggggg cgttgactgg tgaaaatgct     780
ctaaaagcca aggttggcga aactgttcgc ttatttgtgg gtaacggcgg cccgaatttg     840
acatcatcat tccatgtcat tggtgagatt tttgataagg ttcactttga gggtggtaag     900
ggtgaaaacc acaatatcca aaccacgcta atcccagcag gtggcgctgc catcactgaa     960
tttaaggtgg atgtgccggg tgattatgtc ttggttgacc atgccatctt ccgtgccttt    1020
aacaaagggg cattgggcat acttaaggtg gaaggtgaag aaaatcatga gatttattca    1080
cacaaacaaa cagacgctgt ctatctgcca gagggtgccc cacaagcaat tgatacccaa    1140
gaagcaccca aaacacctgc acctgccaac ttacaagagc agattaaagc aggtaaggca    1200
acctatgact ctaactgtgc tgcttgtcac caacctgatg gtaaaggcgt gccaaacgct    1260
ttcccaccgc ttgccaactc tgactatctg aacgccgacc acgctcgtgc cgccagcatc    1320
gtggcaaatg gattgtctgg taagattacc gtcaatggca accaatatga aagcgtcatg    1380
cctgcgattg ctctgagcga ccaacagatt gccaatgtca tcacctacac gcttaacagc    1440
tttggtaaca aaggcggtca actcagtgca gacgatgtgg caaaagccaa aaaaaccaag    1500
ccaaac                                                               1506
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<210> 4
<211> 502
<212> PRT
<213> *Moraxella catarrhalis*

<400> 4

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Met Ser Lys Pro Thr Leu Ile Lys Thr Thr Leu Ile Cys Ala Leu Ser
 1               5                  10                  15
Ala Leu Met Leu Ser Gly Cys Ser Asn Gln Ala Asp Lys Ala Ala Gln
            20                  25                  30
Pro Lys Ser Ser Thr Val Asp Ala Ala Ala Lys Thr Ala Asn Ala Asp
        35                  40                  45
Asn Ala Ala Ser Gln Glu His Gln Gly Glu Leu Pro Val Ile Asp Ala
    50                  55                  60
Ile Val Thr His Ala Pro Glu Val Pro Pro Pro Val Asp Arg Asp His
65                  70                  75                  80
Pro Ala Lys Val Val Val Lys Met Glu Thr Val Glu Lys Val Met Arg
                85                  90                  95
Leu Ala Asp Gly Val Glu Tyr Gln Phe Trp Thr Phe Gly Gly Gln Val
            100                 105                 110
Pro Gly Gln Met Ile Arg Val Arg Glu Gly Asp Thr Ile Glu Val Gln
        115                 120                 125
Phe Ser Asn His Pro Asp Ser Lys Met Pro His Asn Val Asp Phe His
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```
    130                 135                 140
Ala Ala Thr Gly Pro Gly Gly Gly Ala Glu Ala Ser Phe Thr Ala Pro
145                 150                 155                 160
Gly His Thr Ser Thr Phe Ser Phe Lys Ala Leu Gln Pro Gly Leu Tyr
                165                 170                 175
Val Tyr His Cys Ala Val Ala Pro Val Gly Met His Ile Ala Asn Gly
            180                 185                 190
Met Tyr Gly Leu Ile Leu Val Glu Pro Lys Glu Gly Leu Pro Lys Val
        195                 200                 205
Asp Lys Glu Tyr Tyr Val Met Gln Gly Asp Phe Tyr Thr Lys Gly Lys
    210                 215                 220
Tyr Gly Glu Gln Gly Leu Gln Pro Phe Asp Met Glu Lys Ala Ile Arg
225                 230                 235                 240
Glu Asp Ala Glu Tyr Val Val Phe Asn Gly Ser Val Gly Ala Leu Thr
                245                 250                 255
Gly Glu Asn Ala Leu Lys Ala Lys Val Gly Glu Thr Val Arg Leu Phe
            260                 265                 270
Val Gly Asn Gly Gly Pro Asn Leu Thr Ser Ser Phe His Val Ile Gly
        275                 280                 285
Glu Ile Phe Asp Lys Val His Phe Glu Gly Gly Lys Gly Glu Asn His
    290                 295                 300
Asn Ile Gln Thr Thr Leu Ile Pro Ala Gly Gly Ala Ala Ile Thr Glu
305                 310                 315                 320
Phe Lys Val Asp Val Pro Gly Asp Tyr Val Leu Val Asp His Ala Ile
                325                 330                 335
Phe Arg Ala Phe Asn Lys Gly Ala Leu Gly Ile Leu Lys Val Glu Gly
            340                 345                 350
Glu Glu Asn His Glu Ile Tyr Ser His Lys Gln Thr Asp Ala Val Tyr
        355                 360                 365
Leu Pro Glu Gly Ala Pro Gln Ala Ile Asp Thr Gln Glu Ala Pro Lys
    370                 375                 380
Thr Pro Ala Pro Ala Asn Leu Gln Glu Gln Ile Lys Ala Gly Lys Ala
385                 390                 395                 400
Thr Tyr Asp Ser Asn Cys Ala Ala Cys His Gln Pro Asp Gly Lys Gly
                405                 410                 415
Val Pro Asn Ala Phe Pro Pro Leu Ala Asn Ser Asp Tyr Leu Asn Ala
            420                 425                 430
Asp His Ala Arg Ala Ala Ser Ile Val Ala Asn Gly Leu Ser Gly Lys
        435                 440                 445
Ile Thr Val Asn Gly Asn Gln Tyr Glu Ser Val Met Pro Ala Ile Ala
    450                 455                 460
Leu Ser Asp Gln Gln Ile Ala Asn Val Ile Thr Tyr Thr Leu Asn Ser
465                 470                 475                 480
Phe Gly Asn Lys Gly Gly Gln Leu Ser Ala Asp Asp Val Ala Lys Ala
                485                 490                 495
Lys Lys Thr Lys Pro Asn
            500
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<210> 5
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> primer

<400> 5
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<210> 6
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> primer

<400> 6
gggggcgttg actggtgaaa atg 23

<210> 7
<211> 17
<212> DNA
<213> Artificial Sequence

<220>
<223> primer

<400> 7
gtaaaacgac ggccagt 17

<210> 8
<211> 17
<212> DNA
<213> Artificial Sequence

<220>
<223> primer

<400> 8
caggaaacag ctatgac 17

<210> 9
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> primer

<400> 9
acatgtctaa gcctactttg at 22

<210> 10
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> primer

<400> 10
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SEQUENCE LISTING

<110> Joelle Thonnard

<120> Novel Compounds

<130> BM45412

<150> 9921691.3
<151> 1999-09-14

<160> 10

<170> FastSEQ for Windows Version 4.0

<210> 1
<211> 1509
<212> DNA
<213> Moraxella catarrhalis

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gccgccaaga cagcaaatgc agataatgct gcctcacaag aacatcaagg cgagctgcct 180
gtcattgatg ccattgttac gcatgcacca gaagttccac cacctgttga ccgtgaccac 240
cccgccaaag tggtggtaaa aatggaaacc gttgaaaaag tcatgcgtct ggcagatggc 300
gtggaatatc agttttggac atttggcggt caagttccag ggcagatgat tcgtgtgcgt 360
gaaggcgaca ccatcgaagt gcagttctca aaccacccag attcaaaaat gccccataat 420
gttgactttc acgctgccac agggcctggc ggcggggcag aagcgtcatt taccgcaccg 480
ggtcatacat caacctttag ttttaaagcc ttacagcctg gtttgtatgt ctatcactgt 540
gcggttgccc ctgttggcat gcacattgct aatggcatgt atggtttgat tttggttgaa 600
ccaaaagagg gcttgccaaa agtagataaa gaatactatg tcatgcaagg cgacttttat 660
accaaaggca aatatggcga acaaggtcta cagccctttg atatggaaaa agccattcga 720
gaagatgctg aatatgttgt ctttaatggt tcggtggggg cgttgactgg tgaaaatgct 780
ctaaaagcca aggttggcga aactgttcgc ttatttgtgg gtaacggcgg cccgaatttg 840
acatcatcat tccatgtcat tggtgagatt tttgataagg ttcactttga gggtggtaag 900
ggtgaaaacc acaatatcca aaccacgcta atcccagcag gtggcgctgc catcactgaa 960
tttaaggtgg atgtgccggg tgattatgtc ttggttgacc atgccatctt ccgtgccttt 1020
aacaaagggg cattgggcat acttaaggtg gaaggtgaag aaaatcatga gatttattca 1080
cacaaacaaa cagacgctgt ctatctgcca gagggtgccc cacaagcaat tgatacccaa 1140
gaagcaccca aaacacctgc acctgccaac ttacaagagc agattaaagc aggtaaggca 1200
acctatgact ctaactgtgc tgcttgtcac caacctgatg gtaaaggcgt gccaaacgct 1260
ttcccaccgc ttgccaactc tgactatctg aacgccgacc acgctcgtgc cgccagcatc 1320
gtggcaaatg gattgtctgg taagattacc gtcaatggca accaatatga aagcgtcatg 1380
cctgcgattg ctctgagcga ccaacagatt gccaatgtca tcacctacac gcttaacagc 1440
tttggtaaca aaggcggtca actcagtgca gacgatgtgg caaaagccaa aaaaaccaag 1500
ccaaactga 1509

<210> 2
<211> 502
<212> PRT
<213> Moraxella catarrhalis

<400> 2

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Met Ser Lys Pro Thr Leu Ile Lys Thr Thr Leu Ile Cys Ala Leu Ser
 1               5                  10                  15
Ala Leu Met Leu Ser Gly Cys Ser Asn Gln Ala Asp Lys Ala Ala Gln
            20                  25                  30
Pro Lys Ser Ser Thr Val Asp Ala Ala Ala Lys Thr Ala Asn Ala Asp
        35                  40                  45
Asn Ala Ala Ser Gln Glu His Gln Gly Glu Leu Pro Val Ile Asp Ala
    50                  55                  60
Ile Val Thr His Ala Pro Glu Val Pro Pro Pro Val Asp Arg Asp His
65                  70                  75                  80
Pro Ala Lys Val Val Val Lys Met Glu Thr Val Glu Lys Val Met Arg
                85                  90                  95
Leu Ala Asp Gly Val Glu Tyr Gln Phe Trp Thr Phe Gly Gly Gln Val
            100                 105                 110
Pro Gly Gln Met Ile Arg Val Arg Glu Gly Asp Thr Ile Glu Val Gln
        115                 120                 125
Phe Ser Asn His Pro Asp Ser Lys Met Pro His Asn Val Asp Phe His
    130                 135                 140
Ala Ala Thr Gly Pro Gly Gly Gly Ala Glu Ala Ser Phe Thr Ala Pro
145                 150                 155                 160
Gly His Thr Ser Thr Phe Ser Phe Lys Ala Leu Gln Pro Gly Leu Tyr
                165                 170                 175
Val Tyr His Cys Ala Val Ala Pro Val Gly Met His Ile Ala Asn Gly
            180                 185                 190
Met Tyr Gly Leu Ile Leu Val Glu Pro Lys Glu Gly Leu Pro Lys Val
        195                 200                 205
Asp Lys Glu Tyr Tyr Val Met Gln Gly Asp Phe Tyr Thr Lys Gly Lys
    210                 215                 220
Tyr Gly Glu Gln Gly Leu Gln Pro Phe Asp Met Glu Lys Ala Ile Arg
225                 230                 235                 240
Glu Asp Ala Glu Tyr Val Val Phe Asn Gly Ser Val Gly Ala Leu Thr
                245                 250                 255
Gly Glu Asn Ala Leu Lys Ala Lys Val Gly Glu Thr Val Arg Leu Phe
            260                 265                 270
Val Gly Asn Gly Gly Pro Asn Leu Thr Ser Ser Phe His Val Ile Gly
        275                 280                 285
Glu Ile Phe Asp Lys Val His Phe Glu Gly Gly Lys Gly Glu Asn His
    290                 295                 300
Asn Ile Gln Thr Thr Leu Ile Pro Ala Gly Gly Ala Ala Ile Thr Glu
305                 310                 315                 320
Phe Lys Val Asp Val Pro Gly Asp Tyr Val Leu Val Asp His Ala Ile
                325                 330                 335
Phe Arg Ala Phe Asn Lys Gly Ala Leu Gly Ile Leu Lys Val Glu Gly
            340                 345                 350
Glu Glu Asn His Glu Ile Tyr Ser His Lys Gln Thr Asp Ala Val Tyr
        355                 360                 365
Leu Pro Glu Gly Ala Pro Gln Ala Ile Asp Thr Gln Glu Ala Pro Lys
    370                 375                 380
Thr Pro Ala Pro Ala Asn Leu Gln Glu Gln Ile Lys Ala Gly Lys Ala
385                 390                 395                 400
Thr Tyr Asp Ser Asn Cys Ala Ala Cys His Gln Pro Asp Gly Lys Gly
                405                 410                 415
```

```
Val Pro Asn Ala Phe Pro Pro Leu Ala Asn Ser Asp Tyr Leu Asn Ala
            420                 425                 430
Asp His Ala Arg Ala Ala Ser Ile Val Ala Asn Gly Leu Ser Gly Lys
        435                 440                 445
Ile Thr Val Asn Gly Asn Gln Tyr Glu Ser Val Met Pro Ala Ile Ala
    450                 455                 460
Leu Ser Asp Gln Gln Ile Ala Asn Val Ile Thr Tyr Thr Leu Asn Ser
465                 470                 475                 480
Phe Gly Asn Lys Gly Gly Gln Leu Ser Ala Asp Asp Val Ala Lys Ala
                485                 490                 495
Lys Lys Thr Lys Pro Asn
            500
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<210> 3
<211> 1506
<212> DNA
<213> Moraxella catarrhalis

<400> 3

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gccgccaaga cagcaaatgc agataatgct gcctcacaag aacatcaagg cgagctgcct     180
gtcattgatg ccattgttac gcatgcacca gaagttccac cacctgttga ccgtgaccac     240
cccgccaaag tggtggtaaa aatggaaacc gttgaaaaag tcatgcgtct ggcagatggc     300
gtggaatatc agttttggac atttggcggt caagttccag ggcagatgat tcgtgtgcgt     360
gaaggcgaca ccatcgaagt gcagttctca aaccacccag attcaaaaat gccccataat     420
gttgactttc acgctgccac agggcctggc ggcggggcag aagcgtcatt taccgcaccg     480
ggtcatacat caacctttag ttttaaagcc ttacagcctg gtttgtatgt ctatcactgt     540
gcggttgccc ctgttggcat gcacattgct aatggcatgt atggtttgat tttggttgaa     600
ccaaaagagg gcttgccaaa agtagataaa gaatactatg tcatgcaagg cgacttttat     660
accaaaggca aatatggcga acaaggtcta cagccctttg atatggaaaa agccattcga     720
gaagatgctg aatatgttgt ctttaatggt tcggtggggg cgttgactgg tgaaaatgct     780
ctaaaagcca aggttggcga aactgttcgc ttatttgtgg gtaacggcgg cccgaatttg     840
acatcatcat tccatgtcat tggtgagatt tttgataagg ttcactttga gggtggtaag     900
ggtgaaaacc acaatatcca aaccacgcta atcccagcag gtggcgctgc catcactgaa     960
tttaaggtgg atgtgccggg tgattatgtc ttggttgacc atgccatctt ccgtgccttt    1020
aacaaagggg cattgggcat acttaaggtg gaaggtgaag aaaatcatga gatttattca    1080
cacaaacaaa cagacgctgt ctatctgcca gagggtgccc cacaagcaat tgatacccaa    1140
gaagcaccca aaacacctgc acctgccaac ttacaagagc agattaaagc aggtaaggca    1200
acctatgact ctaactgtgc tgcttgtcac caacctgatg gtaaaggcgt gccaaacgct    1260
ttcccaccgc ttgccaactc tgactatctg aacgccgacc acgctcgtgc cgccagcatc    1320
gtggcaaatg gattgtctgg taagattacc gtcaatggca accaatatga aagcgtcatg    1380
cctgcgattg ctctgagcga ccaacagatt gccaatgtca tcacctacac gcttaacagc    1440
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ccaaac                                                               1506
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<210> 4
<211> 502
<212> PRT
<213> Moraxella catarrhalis

<400> 4

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Met Ser Lys Pro Thr Leu Ile Lys Thr Thr Leu Ile Cys Ala Leu Ser
 1               5                  10                  15
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Ala Leu Met Leu Ser Gly Cys Ser Asn Gln Ala Asp Lys Ala Ala Gln
20 25 30
Pro Lys Ser Ser Thr Val Asp Ala Ala Ala Lys Thr Ala Asn Ala Asp
35 40 45
Asn Ala Ala Ser Gln Glu His Gln Gly Glu Leu Pro Val Ile Asp Ala
50 55 60
Ile Val Thr His Ala Pro Glu Val Pro Pro Pro Val Asp Arg Asp His
65 70 75 80
Pro Ala Lys Val Val Val Lys Met Glu Thr Val Glu Lys Val Met Arg
85 90 95
Leu Ala Asp Gly Val Glu Tyr Gln Phe Trp Thr Phe Gly Gly Gln Val
100 105 110
Pro Gly Gln Met Ile Arg Val Arg Glu Gly Asp Thr Ile Glu Val Gln
115 120 125
Phe Ser Asn His Pro Asp Ser Lys Met Pro His Asn Val Asp Phe His
130 135 140
Ala Ala Thr Gly Pro Gly Gly Gly Ala Glu Ala Ser Phe Thr Ala Pro
145 150 155 160
Gly His Thr Ser Thr Phe Ser Phe Lys Ala Leu Gln Pro Gly Leu Tyr
165 170 175
Val Tyr His Cys Ala Val Ala Pro Val Gly Met His Ile Ala Asn Gly
180 185 190
Met Tyr Gly Leu Ile Leu Val Glu Pro Lys Glu Gly Leu Pro Lys Val
195 200 205
Asp Lys Glu Tyr Tyr Val Met Gln Gly Asp Phe Tyr Thr Lys Gly Lys
210 215 220
Tyr Gly Glu Gln Gly Leu Gln Pro Phe Asp Met Glu Lys Ala Ile Arg
225 230 235 240
Glu Asp Ala Glu Tyr Val Val Phe Asn Gly Ser Val Gly Ala Leu Thr
245 250 255
Gly Glu Asn Ala Leu Lys Ala Lys Val Gly Glu Thr Val Arg Leu Phe
260 265 270
Val Gly Asn Gly Gly Pro Asn Leu Thr Ser Ser Phe His Val Ile Gly
275 280 285
Glu Ile Phe Asp Lys Val His Phe Glu Gly Gly Lys Gly Glu Asn His
290 295 300
Asn Ile Gln Thr Thr Leu Ile Pro Ala Gly Gly Ala Ala Ile Thr Glu
305 310 315 320
Phe Lys Val Asp Val Pro Gly Asp Tyr Val Leu Val Asp His Ala Ile
325 330 335
Phe Arg Ala Phe Asn Lys Gly Ala Leu Gly Ile Leu Lys Val Glu Gly
340 345 350
Glu Glu Asn His Glu Ile Tyr Ser His Lys Gln Thr Asp Ala Val Tyr
355 360 365
Leu Pro Glu Gly Ala Pro Gln Ala Ile Asp Thr Gln Glu Ala Pro Lys
370 375 380
Thr Pro Ala Pro Ala Asn Leu Gln Glu Gln Ile Lys Ala Gly Lys Ala
385 390 395 400
Thr Tyr Asp Ser Asn Cys Ala Ala Cys His Gln Pro Asp Gly Lys Gly
405 410 415
Val Pro Asn Ala Phe Pro Pro Leu Ala Asn Ser Asp Tyr Leu Asn Ala
420 425 430
Asp His Ala Arg Ala Ala Ser Ile Val Ala Asn Gly Leu Ser Gly Lys
435 440 445

Ile Thr Val Asn Gly Asn Gln Tyr Glu Ser Val Met Pro Ala Ile Ala
450 455 460
Leu Ser Asp Gln Gln Ile Ala Asn Val Ile Thr Tyr Thr Leu Asn Ser
465 470 475 480
Phe Gly Asn Lys Gly Gly Gln Leu Ser Ala Asp Asp Val Ala Lys Ala
485 490 495
Lys Lys Thr Lys Pro Asn
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